

RAW SEQUENCE LISTING

The Biotechnology Systems Branch of the Scientific and Technical
Information Center (STIC) no errors detected.

Application Serial Number: 10/539,527
Source: IPHO
Date Processed by STIC: 10/3/06

ENTERED



IFWO

RAW SEQUENCE LISTING

DATE: 10/03/2006

PATENT APPLICATION: US/10/539,527

TIME: 10:13:53

Input Set : A:\ENDOC.011APC.txt

Output Set: N:\CRF4\10032006\J539527.raw

4 <110> APPLICANT: GIRARD, Jean-Philippe
 5 AGUILAR, Luc
 6 ERARD, Monique
 7 HARALDSEN, Guttorm
 8 BAEKKEVOLD, Espen
 9 VAEGER, Marjan
 10 BRANDTZAEG, Per
 12 <120> TITLE OF INVENTION: NF-HEV COMPOSITIONS AND METHODS OF USE
 15 <130> FILE REFERENCE: ENDOC.011APC
 C--> 17 <140> CURRENT APPLICATION NUMBER: US/10/539,527
 C--> 17 <141> CURRENT FILING DATE: 2005-06-17
 17 <150> PRIOR APPLICATION NUMBER: US 60/435827
 18 <151> PRIOR FILING DATE: 2002-12-19
 20 <160> NUMBER OF SEQ ID NOS: 49
 22 <170> SOFTWARE: FastSEQ for Windows Version 4.0
 24 <210> SEQ ID NO: 1
 25 <211> LENGTH: 2645
 26 <212> TYPE: DNA
 27 <213> ORGANISM: Homo sapiens
 29 <400> SEQUENCE: 1
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 31 caaagtggaa gaacacagca agcaaagcct tgtgtttcaa gctgggaaaa tcccaacaga 120
 32 aggccaaaga agtttgcccc atgtacttta tgaagctccg ctctggcctt atgataaaaa 180
 33 aggaggcctg ttacttttagg agagaaacca ccaaaaggcc ttactgaaa acaggtagaa 240
 34 agcacaaaag acatctggta ctgcctgcct gtcaacagca gtctactgtg-gagtgtttg 300
 35 cctttggtat atcaggggtc cagaaatata ctagagcact tcatgattca agtatcacag 360
 36 gaatttcacc tattacagag tatcttgctt ctctaagcac atacaatgat caatccatta 420
 37 cttttgcttt ggaggatgaa agttatgaga tatatgttga agactgaaa aaagatgaaa 480
 38 agaaagataa ggtgttactg agttactatg agtctcaaca cccctcaaat gaatcagggtg 540
 39 acggtgttga tggtaagatg ttaatggtaa ccctgagtc tacaagaagac ttctggttgc 600
 40 atgccaacaa caaggaacac tctgtggagc tccataagtg tgaaaaacca ctgccagacc 660
 41 aggcttctt tgtccttcat aatatgcact ccaactgtgt ttcatttgaa tgcaagactg 720
 42 atcctggagt gtttataggt gttaaaggata atcatcttgc tctgattaaa gtagactctt 780
 43 ctgagaattt gtgtactgaa aatatcttgt ttaagctctc tgaaacttag ttgatggaaa 840
 44 cctgtgagtc ttgggttgag tacccaaagt ctaccactgg agaaggaatg agagataaag 900
 45 aaagagacag gtgacatcta agggaaatga agagtgtta gcatgtgtgg aatgttttcc 960
 46 atattatgta taaaaatatt ttttctaact ctccagttat tcttttattt ccctctgtat 1020
 47 aactgcattc tcaatacaag tatcagtata ttaaataagg tatttggtaaa gaaacggtca 1080
 48 acattctaaa gagatacagt ctgaccttta cttttctcta gtttcagtcc agaaagaact 1140
 49 tcatatttag agctaaggcc actgaggaaa gagccatagc ttaagtctct atgtagacag 1200
 50 ggatccattt taaagagcta cttagagaaa taattttcca cagttccaaa cgataggctc 1260
 51 aaacactaga gctgctagta aaaagaagac cagatgcttc acagaattat cattttttca 1320
 52 actggaataa aacaccaggt ttgtttgtag atgtcttag caacactcag agcagatctc 1380

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53 ccttactgtc aggggatatg gaacttcaaa ggcccacatg gcaagccagg taacataaat 1440
54 gtgtgaaaaa gtaaagataa ctaaaaaatt tagaaaaata aatccagtat ttgtaaagt 1500
55 aataaacttca tttctaattg ttttaattttt aaaattctga tttttatata ttgagtttaa 1560
56 gcaaggcatt cttacacgag gaagtgaagt aaattttagt tcagacataa aatttcactt 1620
57 attaggaata tgtaacatgc taaaactttt ttttttttaa agagtactga gtcacaacat 1680
58 gtttttagagc atccaagtac catataatcc aactatcatg gtaaggccag aaatcttcta 1740
59 acctaccaga gcctagatga gacaccgaat taacattaa atttcagtaa ctgactgtcc 1800
60 ctcatgtcca tggcctacca tcccttctga ccctggcttc cagggaccta tgtcttttaa 1860
61 tactcactgt cacattgggc aaagttgctt ctaatcctta tttcccatgt gcacaagtct 1920
62 ttttgtattc cagcttccctg ataacactgc ttactgtgga atattcattt gacatctgtc 1980
63 tcttttcatt tcttttaact accatgccct tgatatatct tttgcacctg ctgaacttca 2040
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65 ttttagataa agctattaat ggcaatatatt ttttgctaaa cgtttttgtt ttttactgtc 2160
66 actagggcaa taaaatttat actcaaccat ataataacat tttttaacta cataaggag 2220
67 tagtttttat tttaaagtct tagcaatttc tattacaact tttcttagac ttaacactta 2280
68 tgataaatga ctaacatagt aacagaatct ttatgaaata tgaccttttc tgaaaataca 2340
69 tactttttaca tttctacttt attgagacct attagatgta agtgctagta gaatataaga 2400
70 taaaagaggc tgagaattac catacaaggg tattacaact gtaaaacaat ttatctttgt 2460
71 ttcattgttc tgtcaataat tgttaacaaa gagataaaaa taagaacaga atgtatatca 2520
72 tcccactctga aaaacactaa ttattgacat gtgcatctgt acaataaaact taaaatgatt 2580
73 attaaataat caaatatatc tactacattg tttatattat tgaataaaagt atattttcca 2640
74 aatgt 2645

76 <210> SEQ ID NO: 2
77 <211> LENGTH: 2486
78 <212> TYPE: DNA
79 <213> ORGANISM: Mus musculus
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83 tcagcagcac cgcaggcgaa gccctggtcc cgccttgcaa aataagaaga tcccaacaga 120
84 agaccaaaga attctgccat gtctactgca tgagactccg ttctggcctc accataagaa 180
85 aggagactag ttatttttagg aaagaaccca cgaaaagata ttcactaaaa tcgggtacca 240
86 agcatgaaga gaacttctct gcctatccac gggattctag gaagagatcc ttgcttgcca 300
87 gtatccaagc atttgctgcg tctgttgaca cattgagcat ccaagggaact tcacttttaa 360
88 cacagtctcc tgcttccctg agtacatata atgaccaatc tgtagtttt gttttggaga 420
89 atggatgtta tgtgatcaat gttgacgact ctggaaaaga ccaagagcaa gaccaggtgc 480
90 tactacgcta ctatgagtct ccctgtcctg caagtcaatc aggcgacggt gtggatggga 540
91 agaagctgat ggtgaacatg agtcccatca aagacacaga catctggctg catgccaacg 600
92 acaaggacta ctccgtggag cttcaaaggg gtgacgtctc gcctccggaa caggccttct 660
93 tegtccttca caaaaagtcc tcggactttg tttcatttga atgcaagaat cttcctggca 720
94 cttacatagg agtaaaagat aaccagctgg ctctagtgga ggagaaagat gagagctgca 780
95 acaatattat gtttaagctc tcgaaaatct aatgcagtaa aacgcctgtg cgttctggg 840
96 tgaatgactt aatgcttcca actgaagaaa gggtaacaga gagaaagaaa gccattcttg 900
97 gcttacgatg ttgtggaatg ttattatgta gaaaacttct tttatttctt tttcttcagc 960
98 tacatgttca atagactcac agatatatga cttacggcgt tggtaaagaa actgaaggag 1020
99 attcagcctt gctctttcct tttctctgcc ttgagtcctg tatgaaatca cactcacgga 1080
100 cttcagaaga gcaggcacca cagtgcattg tttgctttag agaggggtcca tttcaaaaac 1140
101 cttcataaaa acaatgcaaa acaagaaaac aaccgaacaa aaaaaccacc tatttctctg 1200
102 ttctaaacaa atgattgtaa tactagagca gttagtggga ggaccagcta gggggaggat 1260
103 cacctagggg aggaccagct agggggagga ccagctgctg caaagactga ctgtttctca 1320

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104 cttataataa aatgccaaat gcctccgcag atgccccagg caaccctcag atcagccctt 1380
105 tctgtgaaga gtggcggttac ctgtgcttgt ttcccttctta aacttccaat ttttctcttt 1440
106 taacacattt aacattttaac ttttaagcaag ccagcttaca ttaggaagtg aaagacattt 1500
107 tagttcccac ccgtgattga aatcattgac tatatctaac aagcttaaag tctcctgtaa 1560
108 gaactgatca ggatatacac taggacatgc caatagaatg ggatctcatg gtgcagtctg 1620
109 aagccctcca actggagaga cgctaacatc atccttctcg ctgatttcca aggagctatg 1680
110 actttggatg catgcatctg cttggatgag atgtctcggc tgccttgcctt ccttatgcac 1740
111 acgttctgtt cagcttcaca gcagcaatgc tcacgggtga atagcttagc ttagcttctg 1800
112 ccccttcttt ggcttctttg accaccatc ccgtaacggc tctcctactc cctcagcttt 1860
113 ctttctcttt gctctgaagt ctatatgcca acacacttat tccactgtct ttaccctgca 1920
114 ctgcagaatt ttacatctac ctactggtta ccagggtgtc ccctgaacaa ccttcctttg 1980
115 tgttttactg ttattaaagt agtaaatatt gtattcaacc atgtagtaat attttaagcc 2040
116 actaaaaggaa tagttttact tatttagaca acagcaattt ctactacatt tttataagct 2100
117 taaaacttac atgtttttaa acttaaaacg ataaagacaa taacaacatt gatggagtat 2160
118 gatatgacag ttcagaaaagg gtttagctctt atcttccagt cgaggaaaacc tattgtatac 2220
119 aatagctgga ggaatgtatg atcaaagagg ccgggaaccg ccgtgtagga tcgtacggct 2280
120 gtaacaggta taattgtttc attaatgtgt cacagtctta ctgtagagga atgtaaaggc 2340
121 ggaatctgag tcattcctct ggaaaccaca gtgttgactc tgtgaatctg tacgatatct 2400
122 ttaaagtagt aactaagtag tcaaatgtgt tcttgacgtt gttcataact ttgaataaac 2460
123 catttttcaa aaccacgtgt gaccac 2486
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126 <211> LENGTH: 2714
127 <212> TYPE: DNA
128 <213> ORGANISM: Canis familiaris
130 <400> SEQUENCE: 3
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132 tattcaacca cgaaaatccc ccagcaaaag atgaacagtt cagcagacaa ggctttggta 120
133 aaatctccta agctgagaaa atcccaacag aagcctgaag gagtttgcca gatgtacttt 180
134 atgcaactgc gttctggcct tatcatagaa aagacatcct gttacttttag gaaagaaatc 240
135 accaaaaggt attcaccaag aacagctgaa aagtgacaga agcaatgtct ggtattcact 300
136 gcctgtcatc agcagctgaa caaagatttc acctctgatg tccctatgtt acagaaatgt 360
137 tttggaagag ctaatgttcc aagtatccaa gaatattctg cttctctgag cacatacaat 420
138 gatcaatcta ttactttcgt ttttgaggat ggaagttagt agatctatgt agaagacttg 480
139 agaaaaggcc aagagaaaga taagggtgta ttccgttatt atgattccca atccccctca 540
140 catgaaacag gtgatgatgt tgatggccag acgttattgg taaacctgag tcctacaaaa 600
141 gataaagatt ttttgctgca tgccaacaac gaggaacatt ctgtggagct acaaaaaatgt 660
142 gaaaaccaat tgccagacca ggcttcttc ctccttcata ggaagtcttc tgaatgtgtt 720
143 tcattcgaat gtaagaacaa tcctggagtgt tttataggag taaaggataa ccaccttgct 780
144 ttaattaaag taggagacca aactaaggat tcatatatag agaaaacat atttaagctc 840
145 tcttaaattt aatgggatga aaaaagttgt caatcctggg ttgggtagcc cagatagcta 900
146 ctgctgaaga aagaataaga gataaagaga tagacaacat ttaagggaaa taaagagtac 960
147 ttagtatgct atggaatgtt tttcttatta tgtgtaaaat atatttttat aatccttcag 1020
148 ttctgttttt tattaccctt gtctactac atattcaata gtgtattatt aaggagacct 1080
149 cagaaaatat acaacctgac ttttactttt tctacttgct gtcaagaaag agcttaatat 1140
150 ctaattaagc tctgctgaga cctctgggga caaggaaggg ccttaatcca agtttcattt 1200
151 tagacaagga tttcaaaaag ccacatagag acataatttt ccctggttcc aaacaagttc 1260
152 aaacagtaga gctgttggtg aaaagacaat cagctctact tagactgaac atttcacaaa 1320
153 tggataaaaa caccaaattt gtttgaagat tcccaaaatt tcagatactt acacatgtag 1380
154 gcagataata taaatatgtg aaatgacaga gacaattgaa aaaattaaga aaaataaatc 1440

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155 ctgtatttgt aaagtaaata attttacctc taattgtttc atttttaaaa tgctgatttt 1500
156 tatagatgga gttaaattta gcaagacatt cttacattag gaagtaaaat aaattttatc 1560
157 tcagacatat aattgaaatc attgggaata tctcaciaaac taaaacatta ttttaaagca 1620
158 ctgagacaca acatacctta agacatcaaa gtaccatggg atccaagtac catgggtgagg 1680
159 ccacaagtgc ccttatctac tagaacctag attggacaca gcattaacat tacaatttta 1740
160 ataactggct atcccttatg ttcattgtat actgtctttc tgactctatg ctccagggat 1800
161 ctgtaacttg atatacatgt caccctgcac aaaatttctt ataactcttt cttaccatgt 1860
162 gtacaagtgt ttttcttgtc caccttcctg attagctgtt ttactatgga atatttattg 1920
163 acttttcttc cttcatttct tttgaccaac tctgttcttg atatacattt tgtgccccgt 1980
164 gagcttcatt ccatatcacc tgacctctgg acaccaacat attttctat tttgtctctc 2040
165 tgatgtagaa tttcacataa gcctattgat gggaatattt tttattaaac atctttgtat 2100
166 tttacattac taaggtagta aaattttattc tcaacgatat atgatttttc aactactaaa 2160
167 ggaataattt ttgcttattt taagtcttaa attctactat aactttttca taggcttaac 2220
168 attgacaata agtgataaac tagtaacaga atacttatga aatacaactg tttctgaaag 2280
169 tgttggcttt ttaattctaa tttgttgaga tctattggat ataatgatgg tggaacataa 2340
170 gattagaaag gctgagaatt actgagtgag ggtaaacaat tgtaaacaac atagctttca 2400
171 ttacattgtc agttttatta tgaagacaaa aataaaagca gaatatatat catcttctct 2460
172 gaaaaacact aaatgttgac catatgcac tgtatgatat actcgaaatg atttgtttta 2520
173 agtaactaaa tatatttatt acattaaatt ctcaagttct attttttaaa agtatgtgag 2580
174 gccatgatga ttttatcata aaataactat tctgaaattt ttaagtcaaa gcaatcttac 2640
175 cttaatccac tgatgttggt atctggggta ggctcatttg ctggtgattc aaaactaaat 2700
176 aagatattcc aaag 2714

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178 <210> SEQ ID NO: 4

179 <211> LENGTH: 270

180 <212> TYPE: PRT

181 <213> ORGANISM: Homo sapiens

183 <400> SEQUENCE: 4

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185 1 5 10 15
186 Trp Lys Asn Thr Ala Ser Lys Ala Leu Cys Phe Lys Leu Gly Lys Ser
187 20 25 30
188 Gln Gln Lys Ala Lys Glu Val Cys Pro Met Tyr Phe Met Lys Leu Arg
189 35 40 45
190 Ser Gly Leu Met Ile Lys Lys Glu Ala Cys Tyr Phe Arg Arg Glu Thr
191 50 55 60
192 Thr Lys Arg Pro Ser Leu Lys Thr Gly Arg Lys His Lys Arg His Leu
193 65 70 75 80
194 Val Leu Ala Ala Cys Gln Gln Gln Ser Thr Val Glu Cys Phe Ala Phe
195 85 90 95
196 Gly Ile Ser Gly Val Gln Lys Tyr Thr Arg Ala Leu His Asp Ser Ser
197 100 105 110
198 Ile Thr Gly Ile Ser Pro Ile Thr Glu Tyr Leu Ala Ser Leu Ser Thr
199 115 120 125
200 Tyr Asn Asp Gln Ser Ile Thr Phe Ala Leu Glu Asp Glu Ser Tyr Glu
201 130 135 140
202 Ile Tyr Val Glu Asp Leu Lys Lys Asp Glu Lys Lys Asp Lys Val Leu
203 145 150 155 160
204 Leu Ser Tyr Tyr Glu Ser Gln His Pro Ser Asn Glu Ser Gly Asp Gly
205 165 170 175

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206 Val Asp Gly Lys Met Leu Met Val Thr Leu Ser Pro Thr Lys Asp Phe
207          180          185          190
208 Trp Leu His Ala Asn Asn Lys Glu His Ser Val Glu Leu His Lys Cys
209          195          200          205
210 Glu Lys Pro Leu Pro Asp Gln Ala Phe Phe Val Leu His Asn Met His
211          210          215          220
212 Ser Asn Cys Val Ser Phe Glu Cys Lys Thr Asp Pro Gly Val Phe Ile
213 225          230          235          240
214 Gly Val Lys Asp Asn His Leu Ala Leu Ile Lys Val Asp Ser Ser Glu
215          245          250          255
216 Asn Leu Cys Thr Glu Asn Ile Leu Phe Lys Leu Ser Glu Thr
217          260          265          270
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221 <211> LENGTH: 266
222 <212> TYPE: PRT
223 <213> ORGANISM: Mus musculus
225 <400> SEQUENCE: 5
226 Met Arg Pro Arg Met Lys Tyr Ser Asn Ser Lys Ile Ser Pro Ala Lys
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228 Phe Ser Ser Thr Ala Gly Glu Ala Leu Val Pro Pro Cys Lys Ile Arg
229          20          25          30
230 Arg Ser Gln Gln Lys Thr Lys Glu Phe Cys His Val Tyr Cys Met Arg
231          35          40          45
232 Leu Arg Ser Gly Leu Thr Ile Arg Lys Glu Thr Ser Tyr Phe Arg Lys
233 50          55          60
234 Glu Pro Thr Lys Arg Tyr Ser Leu Lys Ser Gly Thr Lys His Glu Glu
235 65          70          75          80
236 Asn Phe Ser Ala Tyr Pro Arg Asp Ser Arg Lys Arg Ser Leu Leu Gly
237          85          90          95
238 Ser Ile Gln Ala Phe Ala Ala Ser Val Asp Thr Leu Ser Ile Gln Gly
239          100          105          110
240 Thr Ser Leu Leu Thr Gln Ser Pro Ala Ser Leu Ser Thr Tyr Asn Asp
241          115          120          125
242 Gln Ser Val Ser Phe Val Leu Glu Asn Gly Cys Tyr Val Ile Asn Val
243          130          135          140
244 Asp Asp Ser Gly Lys Asp Gln Glu Gln Asp Gln Val Leu Leu Arg Tyr
245 145          150          155          160
246 Tyr Glu Ser Pro Cys Pro Ala Ser Gln Ser Gly Asp Gly Val Asp Gly
247          165          170          175
248 Lys Lys Leu Met Val Asn Met Ser Pro Ile Lys Asp Thr Asp Ile Trp
249          180          185          190
250 Leu His Ala Asn Asp Lys Asp Tyr Ser Val Glu Leu Gln Arg Gly Asp
251          195          200          205
252 Val Ser Pro Pro Glu Gln Ala Phe Phe Val Leu His Lys Lys Ser Ser
253          210          215          220
254 Asp Phe Val Ser Phe Glu Cys Lys Asn Leu Pro Gly Thr Tyr Ile Gly
255 225          230          235          240
256 Val Lys Asp Asn Gln Leu Ala Leu Val Glu Glu Lys Asp Glu Ser Cys
257          245          250          255

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RAW SEQUENCE LISTING ERROR SUMMARY
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Please Note:

Use of n and/or Xaa have been detected in the Sequence Listing. Please review the Sequence Listing to ensure that a corresponding explanation is presented in the <220> to <223> fields of each sequence which presents at least one n or Xaa.

Seq#:8; N Pos. 6352,6353,6354,6355,6356,6357,6358,6359,6360,6361,6362,6363
Seq#:8; N Pos. 6364,6365,6366,6367,6368,6369,6370,6371,6372,6373,6374,6375
Seq#:8; N Pos. 6376,6377,6378,6379,6380,6381,6382,6383,6384,6385,6386,6387
Seq#:8; N Pos. 6388,6389,6390,6391,6392,6393,6394,6395,6396,6397,6398,6399
Seq#:8; N Pos. 6400,6401,6402,6403,6404,6405,6406,6407,6408,6409,6410,6411
Seq#:8; N Pos. 6412,6413,6414,6415,6416,6417,6418,6419,6420,6421,6422,6423
Seq#:8; N Pos. 6424,6425,6426,6427,6428,6429,6430,6431,6432,6433,6434,6435
Seq#:8; N Pos. 6436,6437,6438,6439,6440,6441,6442,6443,6444,6445,6446,6447
Seq#:8; N Pos. 6448,6449,6450,6451
Seq#:17; N Pos. 26,27,28,29,30,31,32,33,34,35,36,37,38,39,40,41,42,43,44,45
Seq#:17; N Pos. 46,47,48,49,50,51,52

VERIFICATION SUMMARY

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L:17 M:270 C: Current Application Number differs, Replaced Current Application No
L:17 M:271 C: Current Filing Date differs, Replaced Current Filing Date
L:603 M:258 W: Mandatory Feature missing, <220> Tag not found for SEQ ID#:8
L:609 M:258 W: Mandatory Feature missing, <220> Tag not found for SEQ ID#:8
L:715 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:8 after pos.:6300
L:716 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:8 after pos.:6360
L:717 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:8 after pos.:6420
L:896 M:258 W: Mandatory Feature missing, <220> Tag not found for SEQ ID#:17
L:897 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:17 after pos.:0